

#

SEQUENCE LISTING

<110> Forschungszentrum Juelich GmbH

<120> NUCLEOTIDE SEQUENCES THAT ENCODE CORYNEFORM BACTERIA FOR PROTEINS
PARTICIPATING IN THE BIOSYNTHESIS OF L-SERINE AND METHOD OF
PRODUCING
L-SERINE

<130> 23155

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Corynebacterium glutamicum

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<213> Corynebacterium glutamicum

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<213> Corynebacterium glutamicum

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<213> *Corynebacterium glutamicum*

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Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
 225 230 235 240
 Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
 245 250 255
 Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
 260 265 270
 Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
 275 280 285
 Glu Ala Gln Asp Arg Ala Gly Thr Asp Val Ala Asp Ser Val Leu Lys
 290 295 300
 Ala Leu Ala Gly Glu Phe Val Ala Asp Ala Val Asn Val Ser Gly Gly
 305 310 315 320
 Arg Val Gly Glu Glu Val Ala Val Trp Met Asp Leu Ala Arg Lys Leu
 325 330 335
 Gly Leu Leu Ala Gly Lys
 340

<210> 10
 <211> 325
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 10
 Met Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala
 1 5 10 15
 Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val
 20 25 30
 Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp
 35 40 45
 Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
 50 55 60
 Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
 65 70 75 80
 Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
 85 90 95
 Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu
 100 105 110
 Leu Leu Ser Thr Ala Arg Gln Ile Pro Ala Ala Asp Ala Thr Leu Arg
 115 120 125
 Glu Gly Glu Trp Lys Arg Ser Ser Phe Asn Gly Val Glu Ile Phe Gly
 130 135 140
 Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
 145 150 155 160

Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
 165 170 175
 Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
 180 185 190
 Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
 195 200 205
 Thr Lys Glu Thr Ala Gly Met Phe Asp Ala Gln Leu Leu Ala Lys Ser
 210 215 220
 Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
 225 230 235 240
 Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
 245 250 255
 Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
 260 265 270
 Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
 275 280 285
 Glu Ala Gln Asp Arg Ala Gly Thr Asp Val Ala Asp Ser Val Leu Lys
 290 295 300
 Ala Leu Ala Gly Glu Phe Val Ala Asp Ala Val Asn Val Ser Gly Gly
 305 310 315 320
 Arg Val Gly Glu Glu
 325

<210> 11
 <211> 319
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 11
 Met Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala
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 Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val
 20 25 30
 Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp
 35 40 45
 Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
 50 55 60
 Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
 65 70 75 80
 Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
 85 90 95
 Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu

100					105					110					
Leu	Leu	Ser	Thr	Ala	Arg	Gln	Ile	Pro	Ala	Ala	Asp	Ala	Thr	Leu	Arg
		115					120					125			
Glu	Gly	Glu	Trp	Lys	Arg	Ser	Ser	Phe	Asn	Gly	Val	Glu	Ile	Phe	Gly
	130					135					140				
Lys	Thr	Val	Gly	Ile	Val	Gly	Phe	Gly	His	Ile	Gly	Gln	Leu	Phe	Ala
145					150					155					160
Gln	Arg	Leu	Ala	Ala	Phe	Glu	Thr	Thr	Ile	Val	Ala	Tyr	Asp	Pro	Tyr
				165					170					175	
Ala	Asn	Pro	Ala	Arg	Ala	Ala	Gln	Leu	Asn	Val	Glu	Leu	Val	Glu	Leu
			180					185					190		
Asp	Glu	Leu	Met	Ser	Arg	Ser	Asp	Phe	Val	Thr	Ile	His	Leu	Pro	Lys
		195					200					205			
Thr	Lys	Glu	Thr	Ala	Gly	Met	Phe	Asp	Ala	Gln	Leu	Leu	Ala	Lys	Ser
	210					215					220				
Lys	Lys	Gly	Gln	Ile	Ile	Ile	Asn	Ala	Ala	Arg	Gly	Gly	Leu	Val	Asp
225					230					235					240
Glu	Gln	Ala	Leu	Ala	Asp	Ala	Ile	Glu	Ser	Gly	His	Ile	Arg	Gly	Ala
				245					250					255	
Gly	Phe	Asp	Val	Tyr	Ser	Thr	Glu	Pro	Cys	Thr	Asp	Ser	Pro	Leu	Phe
			260					265					270		
Lys	Leu	Pro	Gln	Val	Val	Val	Thr	Pro	His	Leu	Gly	Ala	Ser	Thr	Glu
		275					280					285			
Glu	Ala	Gln	Asp	Arg	Ala	Gly	Thr	Asp	Val	Ala	Asp	Ser	Val	Leu	Lys
	290					295					300				
Ala	Leu	Ala	Gly	Glu	Phe	Val	Ala	Asp	Ala	Val	Asn	Val	Ser	Gly	
305					310					315					

<210> 12
 <211> 530
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 12
 Met Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala
 1 5 10 15
 Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val
 20 25 30
 Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp
 35 40 45
 Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
 50 55 60

Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
 65 70 75 80
 Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
 85 90 95
 Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu
 100 105 110
 Leu Leu Ser Thr Ala Arg Gln Ile Pro Ala Ala Asp Ala Thr Leu Arg
 115 120 125
 Glu Gly Glu Trp Lys Arg Ser Ser Phe Asn Gly Val Glu Ile Phe Gly
 130 135 140
 Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
 145 150 155 160
 Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
 165 170 175
 Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
 180 185 190
 Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
 195 200 205
 Thr Lys Glu Thr Ala Gly Met Phe Asp Ala Gln Leu Leu Ala Lys Ser
 210 215 220
 Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
 225 230 235 240
 Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
 245 250 255
 Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
 260 265 270
 Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
 275 280 285
 Glu Ala Gln Asp Arg Ala Gly Thr Asp Val Ala Asp Ser Val Leu Lys
 290 295 300
 Ala Leu Ala Gly Glu Phe Val Ala Asp Ala Val Asn Val Ser Gly Gly
 305 310 315 320
 Arg Val Gly Glu Glu Val Ala Val Trp Met Asp Leu Ala Arg Lys Leu
 325 330 335
 Gly Leu Leu Ala Gly Lys Leu Val Asp Ala Ala Pro Val Ser Ile Glu
 340 345 350
 Val Glu Ala Arg Gly Glu Leu Ser Ser Glu Gln Val Asp Ala Leu Gly
 355 360 365
 Leu Ser Ala Val Arg Gly Leu Phe Ser Gly Ile Ile Glu Glu Ser Val
 370 375 380
 Thr Phe Val Asn Ala Pro Arg Ile Ala Glu Glu Arg Gly Leu Asp Ile

385 390 395 400
 Ser Val Lys Thr Asn Ser Glu Ser Val Thr His Arg Ser Val Leu Gln
 405 410 415
 Val Lys Val Ile Thr Gly Ser Gly Ala Ser Ala Thr Val Val Gly Ala
 420 425 430
 Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile Asn Gly Arg
 435 440 445
 Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu Gln Tyr Thr
 450 455 460
 Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu Gly Ala Ala
 465 470 475 480
 Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu Lys Gly Asp
 485 490 495
 Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser Glu Glu Leu
 500 505 510
 Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe Gln Val Asp
 515 520 525
 Leu Asp
 530

<210> 13
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic Construct

 <400> 13

tctagagccg gagacgtgaa taaaat 26

<210> 14
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic Construct

 <400> 14

ggatccgact ggtgagggtc aagtcc 26

<210> 15
 <211> 27
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Construct

<400> 15

ggatccttaa ccggaacgt tcacagc

27

<210> 16

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Construct

<400> 16

ggatccttac tcttcgcca cgcgacc

27

<210> 17

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Construct

<400> 17

ggatacctta agccagaatc catccacaca g

31

<210> 18

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Construct

<400> 18

ggatccttac ttgccagcaa gaaaagacc

29

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Construct

<400> 19

ggatccttaa tccaggccac ggccatt

27